

## SEQUENCE LISTING

<110> Klee, Harry J.  
Lashbrook, Coralie  
Shrode, Lori

<120> Materials and Methods for Tissue-Specific Targeting of Ethylene  
Insensitivity in Transgenic Plants

<130> UF-325XC1

<150> US 60/390,385  
<151> 2002-06-21

<160> 9

<170> PatentIn version 3.2

<210> 1  
<211> 738  
<212> PRT  
<213> pLBS107 construct

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Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr  
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Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val  
35 40 45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu  
50 55 60

Tyr Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser  
65 70 75 80

Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val  
85 90 95

Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu  
100 105 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu  
115 120 125

Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg  
130 135 140

His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His  
145 150 155 160

Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu  
 165 170 175

Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln  
 180 185 190

Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro  
 195 200 205

Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val  
 210 215 220

Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly  
 225 230 235 240

Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His  
 245 250 255

Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg  
 260 265 270

Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp  
 275 280 285

His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala  
 290 295 300

Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg  
 305 310 315 320

Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu  
 325 330 335

Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn  
 340 345 350

His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu  
 355 360 365

Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr  
 370 375 380

Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu  
 385 390 395 400

Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr  
 405 410 415

Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro  
 420 425 430

Ile Ala Val Val Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp  
 435 440 445

Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile

450	455	460
Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile		
465	470	475
480		
Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe		
485	490	495
Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys Val Lys		
500	505	510
Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile Phe Thr		
515	520	525
Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser		
530	535	540
Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly		
545	550	555
560		
Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile		
565	570	575
Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln		
580	585	590
Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr		
595	600	605
Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val		
610	615	620
Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser		
625	630	635
640		
Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val		
645	650	655
Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu		
660	665	670
Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu		
675	680	685
Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met		
690	695	700
Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn		
705	710	715
720		
Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu		
725	730	735
Gly Met		

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<212> PRT  
<213> pLBS107 construct

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Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu  
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Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr  
20 25 30

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val  
35 40 45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu  
50 55 60

Tyr Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser  
65 70 75 80

Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val  
85 90 95

Val Ser Cys Ala Thr Thr Leu Met Leu Val His Ile Ile Pro Asp Leu  
100 105 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu  
115 120 125

Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg  
130 135 140

His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His  
145 150 155 160

Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu  
165 170 175

Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln  
180 185 190

Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro  
195 200 205

Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val  
210 215 220

Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly  
225 230 235 240

Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His  
245 250 255

Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg  
 260 265 270

Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp  
 275 280 285

His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala  
 290 295 300

Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg  
 305 310 315 320

Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu  
 325 330 335

Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn  
 340 345 350

His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu  
 355 360 365

Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr  
 370 375 380

Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu  
 385 390 395 400

Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr  
 405 410 415

Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro  
 420 425 430

Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp  
 435 440 445

Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile  
 450 455 460

Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile  
 465 470 475 480

Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe  
 485 490 495

Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys Val Lys  
 500 505 510

Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile Phe Thr  
 515 520 525

Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser  
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Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly  
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Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile  
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Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln  
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Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr  
 595                    600                    605

Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val  
 610                    615                    620

Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser  
 625                    630                    635                    640

Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val  
 645                    650                    655

Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu  
 660                    665                    670

Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu  
 675                    680                    685

Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met  
 690                    695                    700

Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn  
 705                    710                    715                    720

Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu  
 725                    730                    735

Gly Met

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Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Val Tyr  
 20                    25                    30

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val  
 35                    40                    45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu  
 50 55 60

Tyr Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser  
 65 70 75 80

Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val  
 85 90 95

Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu  
 100 105 110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu  
 115 120 125

Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg  
 130 135 140

His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His  
 145 150 155 160

Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu  
 165 170 175

Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln  
 180 185 190

Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro  
 195 200 205

Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val  
 210 215 220

Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly  
 225 230 235 240

Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His  
 245 250 255

Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg  
 260 265 270

Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp  
 275 280 285

His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala  
 290 295 300

Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg  
 305 310 315 320

Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu  
 325 330 335

Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn

340	345	350
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His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu		
355	360	365

Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr		
370	375	380

Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu		
385	390	395
		400

Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr		
405	410	415

Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro		
420	425	430

Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp		
435	440	445

Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile		
450	455	460

Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile		
465	470	475
		480

Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe		
485	490	495

Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys Val Lys		
500	505	510

Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile Phe Thr		
515	520	525

Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser		
530	535	540

Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly		
545	550	555
		560

Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile		
565	570	575

Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln		
580	585	590

Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr		
595	600	605

Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val		
610	615	620

Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser		
625	630	635
		640

Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val  
 645                        650                        655

Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu  
 660                        665                        670

Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu  
 675                        680                        685

Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met  
 690                        695                        700

Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn  
 705                        710                        715                        720

Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu  
 725                        730                        735

Gly Met

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Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu  
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Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr  
 20                        25                        30

Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val  
 35                        40                        45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Phe Val Leu  
 50                        55                        60

Tyr Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser  
 65                        70                        75                        80

Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val  
 85                        90                        95

Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu  
 100                      105                        110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu  
 115                      120                        125

Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg  
 130                      135                        140

His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His  
 145 150 155 160  
 Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu  
 165 170 175  
 Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln  
 180 185 190  
 Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro  
 195 200 205  
 Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val  
 210 215 220  
 Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly  
 225 230 235 240  
 Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His  
 245 250 255  
 Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg  
 260 265 270  
 Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp  
 275 280 285  
 His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala  
 290 295 300  
 Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg  
 305 310 315 320  
 Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu  
 325 330 335  
 Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn  
 340 345 350  
 His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu  
 355 360 365  
 Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr  
 370 375 380  
 Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu  
 385 390 395 400  
 Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr  
 405 410 415  
 Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro  
 420 425 430

Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp  
 435                    440                    445

Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile  
 450                    455                    460

Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile  
 465                    470                    475                    480

Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe  
 485                    490                    495

Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys Val Lys  
 500                    505                    510

Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile Phe Thr  
 515                    520                    525

Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser  
 530                    535                    540

Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly  
 545                    550                    555                    560

Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile  
 565                    570                    575

Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln  
 580                    585                    590

Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr  
 595                    600                    605

Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val  
 610                    615                    620

Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser  
 625                    630                    635                    640

Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val  
 645                    650                    655

Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu  
 660                    665                    670

Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu  
 675                    680                    685

Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met  
 690                    695                    700

Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn  
 705                    710                    715                    720

Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu

725

730

735

## Gly Met

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Met Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu					
1	5	10		15	
tta atg aaa tac caa tac atc tcc gat ttc ttc att gcg att gcg tat					96
Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ala Tyr					
20	25		30		
ttt tcg att cct ctt gag ttg att tac ttt gtg aag aaa tca gcc gtg					144
Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val					
35	40		45		
ttt ccg tat aga tgg gta ctt gtt cag ttt ggt gct ttt atc gtt ctt					192
Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu					
50	55		60		
tat gga gca act cat ctt att aac tta tgg act ttc act acg cat tcg					240
Tyr Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser					
65	70	75		80	
aga acc gtg gcg ctt gtg atg act acc gcg aag gtg tta acc gct gtt					288
Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val					
85	90		95		
gtc tcg tgt gct act gcg ttg atg ctt gtt cat att att cct gat ctt					336
Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu					
100	105		110		
ttg agt gtt aag act cgg gag ctt ttc ttg aaa aat aaa gct gct gag					384
Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu					
115	120		125		
ctc gat aga gaa atg gga ttg att cga act cag gaa acc gga agg					432
Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg					
130	135		140		
cat gtg aga atg ttg act cat gag att aga agc act tta gat aga cat					480
His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His					
145	150	155		160	

act att tta aag act aca ctt gtt gag ctt ggt agg aca tta gct ttg		528
Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu		
165	170	175
gag gag tgt gca ttg tgg atg cct act aga act ggg tta gag cta cag		576
Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln		
180	185	190
ctt tct tat aca ctt cgt cat caa cat ccc gtg gag tat acg gtt cct		624
Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro		
195	200	205
att caa tta ccg gtg att aac caa gtg ttt ggt act agt agg gct gta		672
Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val		
210	215	220
aaa ata tct cct aat tct cct gtg gct agg ttg aga cct gtt tct ggg		720
Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly		
225	230	235
240		
aaa tat atg cta ggg gag gtg gtc gct gtg agg gtt ccg ctt ctc cac		768
Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His		
245	250	255
ctt tct aat ttt cag att aat gac tgg cct gag ctt tca aca aag aga		816
Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg		
260	265	270
tat gct ttg atg gtt ttg atg ctt cct tca gat agt gca agg caa tgg		864
Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp		
275	280	285
cat gtc cat gag ttg gaa ctc gtt gaa gtc gtc gct gat cag gtg gct		912
His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala		
290	295	300
300		
gta gct ctc tca cat gct gcg atc cta gaa gag tcg atg cga gct agg		960
Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg		
305	310	315
320		
gac ctt ctc atg gag cag aat gtt gct ctt gat cta gct aga cga gaa		1008
Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu		
325	330	335
335		
gca gaa aca gca atc cgt gcc cgc aat gat ttc cta gcg gtt atg aac		1056
Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn		
340	345	350
350		
cat gaa atg cga aca ccg atg cat gcg att att gca ctc tct tcc tta		1104
His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu		
355	360	365
365		
ctc caa gaa acg gaa cta acc cct gaa caa aga ctg atg gtg gaa aca		1152
Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr		
370	375	380
380		

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gat ctt tca agg tta gaa gat gga agt ctt caa ctt gaa ctt ggg aca Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr 405 410 415	1248
ttc aat ctt cat aca tta ttt aga gag gtc ctc aat ctg ata aag cct Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro 420 425 430	1296
ata gcg gtt gtt aag aaa tta ccc atc aca cta aat ctt gca cca gat Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp 435 440 445	1344
ttg cca gaa ttt gtt gtt ggg gat gag aaa cggt cta atg cag ata ata Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile 450 455 460	1392
tta aat ata gtt ggt aat gct gtg aaa ttc tcc aaa caa ggt agt atc Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile 465 470 475 480	1440
tcc gta acc gct ctt gtc acc aag tca gac aca cga gct gct gac ttt Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe 485 490 495	1488
ttt gtc gtg cca act ggg agt cat ttc tac ttg aga gtg aag gta aaa Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys Val Lys 500 505 510	1536
gac tct gga gca gga ata aat cct caa gac att cca aag att ttc act Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile Phe Thr 515 520 525	1584
aaa ttt gct caa aca caa tct tta gcg acg aga agc tcg ggt ggt agt Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser 530 535 540	1632
ggg ctt ggc ctc gcc atc tcc aag agg ttt gtg aat ctg atg gag ggt Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly 545 550 555 560	1680
aac att tgg att gag agc gat ggt ctt gga aaa gga tgc acg gct atc Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Cys Thr Ala Ile 565 570 575	1728
ttt gat gtt aaa ctt ggg atc tca gaa cgt tca aac gaa tct aaa cag Phe Asp Val Lys Leu Gly Ile Ser Gln Arg Ser Asn Glu Ser Lys Gln 580 585 590	1776
tcg ggc ata ccg aaa gtt cca gcc att ccc cga cat tca aat ttc act Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr	1824

595	600	605	
gga ctt aag gtt ctt gtc atg gat gag aac ggg gta agt aga atg gtg Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val			1872
610	615	620	
acg aag gga ctt ctt gta cac ctt ggg tgc gaa gtg acc acg gtg agt Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser			1920
625	630	635	640
tca aac gag gag tgt ctc cga gtt gtg tcc cat gag cac aaa gtg gtc Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val			1968
645	650	655	
ttc atg gac gtg tgc atg ccc ggg gtc gaa aac tac caa atc gct ctc Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu			2016
660	665	670	
cgt att cac gag aaa ttc aca aaa caa cgc cac caa cgg cca cta ctt Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu			2064
675	680	685	
gtg gca ctc agt ggt aac act gac aaa tcc aca aaa gag aaa tgc atg Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met			2112
690	695	700	
agc ttt ggt cta gac ggt gtg ttg ctc aaa ccc gta tca cta gac aac Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn			2160
705	710	715	720
ata aga gat gtt ctg tct gat ctt ctc gag ccc cgg gta ctg tac gag Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu			2208
725	730	735	
ggc atg			2214

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<213> Amino acid sequence alignment of ETR2

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Phe Val Ser Pro Val Leu Ala Ile Asn Gly Gly Tyr Pro Arg Cys  
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Asn Cys Glu Asp Glu Gly Asn Ser Phe Trp Ser Thr Glu Asn Ile Leu  
35 40 45

Glu Thr Gln Arg Val Ser Asp Phe Leu Ile Ala Val Ala Tyr Phe Ser  
50 55 60

Ile Pro Ile Glu Leu Leu Tyr Phe Val Ser Cys Ser Asn Val Pro Phe  
 65 70 75 80

Lys Trp Val Leu Phe Glu Phe Ile Ala Phe Ile Val Leu Cys Gly Met  
 85 90 95

Thr His Leu Leu His Gly Trp Thr Tyr Ser Ala His Pro Phe Arg Leu  
 100 105 110

Met Met Ala Phe Thr Val Phe Lys Met Leu Thr Ala Leu Val Ser Cys  
 115 120 125

Ala Thr Ala Ile Thr Leu Ile Thr Leu Ile Pro Leu Leu Lys Val  
 130 135 140

Lys Val Arg Glu Phe Met Leu Lys Lys Ala His Glu Leu Gly Arg  
 145 150 155 160

Glu Val Gly Leu Ile Leu Ile Lys Lys Glu Thr Gly Phe His Val Arg  
 165 170 175

Met Leu Thr Gln Glu Ile Arg Lys Ser Leu Asp Arg His Thr Ile Leu  
 180 185 190

Tyr Thr Thr Leu Val Glu Leu Ser Lys Thr Leu Gly Leu Gln Asn Cys  
 195 200 205

Ala Val Trp Met Pro Asn Asp Gly Gly Thr Glu Met Asp Leu Thr His  
 210 215 220

Glu Leu Arg Gly Arg Gly Gly Tyr Gly Gly Cys Ser Val Ser Met Glu  
 225 230 235 240

Asp Leu Asp Val Val Arg Ile Arg Glu Ser Asp Glu Val Asn Val Leu  
 245 250 255

Ser Val Asp Ser Ser Ile Ala Arg Ala Ser Gly Gly Gly Asp Val  
 260 265 270

Ser Glu Ile Gly Ala Val Ala Ala Ile Arg Met Pro Met Leu Arg Val  
 275 280 285

Ser Asp Phe Asn Gly Glu Leu Ser Tyr Ala Ile Leu Val Cys Val Leu  
 290 295 300

Pro Gly Gly Thr Pro Arg Asp Trp Thr Tyr Gln Glu Ile Glu Ile Val  
 305 310 315 320

Lys Val Val Ala Asp Gln Val Thr Val Ala Leu Asp His Ala Ala Val  
 325 330 335

Leu Glu Glu Ser Gln Leu Met Arg Glu Lys Leu Ala Glu Gln Asn Arg  
 340 345 350

Ala Leu Gln Met Ala Lys Arg Asp Ala Leu Arg Ala Ser Gln Ala Arg  
 355                   360                   365

Asn Ala Phe Gln Lys Thr Met Ser Glu Gly Met Arg Arg Pro Met His  
 370                   375                   380

Ser Ile Leu Gly Leu Leu Ser Met Ile Gln Asp Glu Lys Leu Ser Asp  
 385                   390                   395                   400

Glu Gln Lys Met Ile Val Asp Thr Met Val Lys Thr Gly Asn Val Met  
 405                   410                   415

Ser Asn Leu Val Gly Asp Ser Met Asp Val Pro Asp Gly Arg Phe Gly  
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Thr Glu Met Lys Pro Phe Ser Leu His Arg Thr Ile His Glu Ala Ala  
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Cys Met Ala Arg Cys Leu Cys Leu Cys Asn Gly Ile Arg Phe Leu Val  
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Asp Ala Glu Lys Ser Leu Pro Asp Asn Val Val Gly Asp Glu Arg Arg  
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Val Phe Gln Val Ile Leu His Ile Val Gly Ser Leu Val Lys Pro Arg  
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Lys Arg Gln Glu Gly Ser Ser Leu Met Phe Lys Val Leu Lys Glu Arg  
 500                   505                   510

Gly Ser Leu Asp Arg Ser Asp His Arg Trp Ala Ala Trp Arg Ser Pro  
 515                   520                   525

Ala Ser Ser Ala Asp Gly Asp Val Tyr Ile Arg Phe Glu Met Asn Val  
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Glu Asn Asp Asp Ser Ser Ser Gln Ser Phe Ala Ser Val Ser Ser Arg  
 545                   550                   555                   560

Asp Gln Glu Val Gly Asp Val Arg Phe Ser Gly Gly Tyr Gly Leu Gly  
 565                   570                   575

Gln Asp Leu Ser Phe Gly Val Cys Lys Lys Val Val Gln Leu Ile His  
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Gly Asn Ile Ser Val Val Pro Gly Ser Asp Gly Ser Pro Glu Thr Met  
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Ser Leu Leu Leu Arg Phe Arg Arg Arg Pro Ser Ile Ser Val His Gly  
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Ser Ser Glu Ser Pro Ala Pro Asp His His Ala His Pro His Ser Asn  
 625                   630                   635                   640

Ser Leu Leu Arg Gly Leu Gln Val Leu Leu Val Asp Thr Asn Asp Ser

645

650

655

Asn Arg Ala Val Thr Arg Lys Leu Leu Glu Lys Leu Gly Cys Asp Val  
 660 665 670

Thr Ala Val Ser Ser Gly Phe Asp Cys Leu Thr Ala Ile Ala Pro Gly  
 675 680 685

Ser Ser Ser Pro Ser Thr Ser Phe Gln Val Val Val Leu Asp Leu Gln  
 690 695 700

Met Ala Glu Met Asp Gly Tyr Glu Val Ala Met Arg Ile Arg Ser Arg  
 705 710 715 720

Ser Trp Pro Leu Ile Val Ala Thr Thr Val Ser Leu Asp Glu Glu Met  
 725 730 735

Trp Asp Lys Cys Ala Gln Ile Gly Ile Asn Gly Val Val Arg Lys Pro  
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Val Val Leu Arg Ala Met Glu Ser Glu Leu Arg Arg Val Leu Leu Gln  
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Ala Asp Gln Leu Leu  
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<211> 2893  
<212> DNA  
<213> Amino acid sequence alignment of ETR2

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gagaggaaga tcggaatgtc gaagagaatt agaagattct cgtacatcac ttcgttgaa	300
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tatccacgat gtaactgcga agacgaagga aacagttct ggagtacaga gaacattcta	540
gaaactcaa gagtaagcga tttcttaatc gcagtagctt atttctcaat ccctattgag	600
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gttggtagtt tagtaaagcc tagaaaacgt caagaaggat cttcattgtat gtttaagggtt	1920
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gcttcattcag cagatggaga tggatata agatttggaa tgaatgtaga gaatgtatgtat	2040
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gctgaccaac ttctctaagt tgttatctca acttctcttc tacattcaaa atttttacac	2760
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atcaactggag gtaaacaaaa agaaaggtaa agaaaggctc ctaatcagat gaaaatttct	180
ctcaaaacttt tagcactctt ttggAACGTA aacagtgaag tgaacttagag atgttaaaag	240
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aattcaatcc tttgaattgt taaatatata atatatgttt aatgtcttcc tgTTTAACC	360
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agTTTaaa aatacgTTaa aagaaatgga taagggagga aaacagaggg aaaAGCAGAA	1020
gaggatgaaa gaaaaagaaa gTTaaaagaa cataaaagaa aaaattaaat tgctctaaa	1080
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acttgagata aataaaagtt gCTATTAAA TTtaggtata tcaacattaa taatgttggc	1320
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aacccttaat ttccaacttt tagttggtga ggataagatg agactaaaat ccgacattgc	1440
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aagtccACCT ttttaatca aaactacaac agtgaaggaa actacgaata atctatcatt	1560
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ca	1622

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 <212> DNA  
 <213> pLBS107 construct

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atcaCTGGAG gtaaacAAAA agaaAGGTaa agaaAGGCTC ctaatcAGAT gaaaatttCT	180
ctcaaACTTT tagcactCTT ttggAACGTA AACAGTGAAG tgaACTAGAG atgttAAAG	240
aggaAGATAA atggTAAAT atacAAATG tggtaACAT aaatCCATT atccccCATT	300
aattcaATCC tttGAATTGT taaatatata atatATGTT aatgtcttcc tggTTAACC	360
atggtaAAGG agtcttCTTG atttGTTAAT taagtGAAAG gcaccaAAAC caaatttATA	420

22

UF-325XC1

gcgtttaat tgagtacatt ttgtatatac ggtcgaaagc cgcctcaggg ttcaatggct	480
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gttcgaacct ttttaatt tgcaatgtaa ttatttgct tatgttacat tttagtcatt	660
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gaggatgaaa gaaaaagaaa gttaaaagaa cataaaagaa aaaattaaat tgctctaaaa	1080
gaaaaaatat ggggacagat tgtataaatt agccaaaaat tttgtttaa aatgatgatt	1140
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gaa gtc tgc aat tgt att gaa ccg caa tgg cca gcg gat gaa ttg tta Glu Val Cys Asn Cys Ile Glu Pro Gln Trp Pro Ala Asp Glu Leu Leu 5 10 15	1724
atg aaa tac caa tac atc tcc gat ttc ttc att gcg att gcg tat ttt Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr Phe 20 25 30	1772
tcg att cct ctt gag ttg att tac ttt gtg aag aaa tca gcc gtg ttt Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val Phe 35 40 45	1820

ccg tat aga tgg gta ctt gtt cag ttt ggt gct ttt atc gtt ctt tat Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu Tyr 50 55 60 65	1868
gga gca act cat ctt att aac tta tgg act ttc act acg cat tcg aga Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser Arg 70 75 80	1916
acc gtg gcg ctt gtg atg act acc gcg aag gtg tta acc gct gtt gtc Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val Val 85 90 95	1964
tcg tgt gct act gcg ttg atg ctt gtt cat att att cct gat ctt ttg Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu Leu 100 105 110	2012
agt gtt aag act cgg gag ctt ttc ttg aaa aat aaa gct gct gag ctc Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu Leu 115 120 125	2060
gat aga gaa atg gga ttg att cga act cag gaa gaa acc gga agg cat Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg His 130 135 140 145	2108
gtg aga atg ttg act cat gag att aga agc act tta gat aga cat act Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His Thr 150 155 160	2156
att tta aag act aca ctt gtt gag ctt ggt agg aca tta gct ttg gag Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu Glu 165 170 175	2204
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caa tta ccg gtg att aac caa gtg ttt ggt act agt agg gct gta aaa Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val Lys 210 215 220 225	2348
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260	265	270	
gct ttg atg gtt ttg atg ctt cct tca gat agt gca agg caa tgg cat Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp His 275	280	285	2540
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gct ctc tca cat gct gcg atc cta gaa gag tcg atg cga gct agg gac Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg Asp 310	315	320	2636
ctt ctc atg gag cag aat gtt gct ctt gat cta gct aga cga gaa gca Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu Ala 325	330	335	2684
gaa aca gca atc cgt gcc cgc aat gat ttc cta gcg gtt atg aac cat Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His 340	345	350	2732
gaa atg cga aca ccg atg cat gcg att att gca ctc tct tcc tta ctc Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu Leu 355	360	365	2780
caa gaa acg gaa cta acc cct gaa caa aga ctg atg gtg gaa aca ata Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr Ile 370	375	380	2828
ctt aaa agt agt aac ctt ttg gca act ttg atg aat gat gtc tta gat Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu Asp 390	395	400	2876
ctt tca agg tta gaa gat gga agt ctt caa ctt gaa ctt ggg aca ttc Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr Phe 405	410	415	2924
aat ctt cat aca tta ttt aga gag gtc ctc aat ctg ata aag cct ata Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro Ile 420	425	430	2972
gcg gtt gtt aag aaa tta ccc atc aca cta aat ctt gca cca gat ttg Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp Leu 435	440	445	3020
cca gaa ttt gtt gtt ggg gat gag aaa cgg cta atg cag ata ata tta Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile Leu 450	455	460	3068
aat ata gtt ggt aat gct gtg aaa ttc tcc aaa caa ggt agt atc tcc Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile Ser 470	475	480	3116
gta acc gct ctt gtc acc aag tca gac aca cga gct gct gac ttt ttt			3164

Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe Phe			
485	490	495	
gtc gtg cca act ggg agt cat ttc tac ttg aga gtg aag gta aaa gac			3212
Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys Val Lys Asp			
500	505	510	
tct gga gca gga ata aat cct caa gac att cca aag att ttc act aaa			3260
Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile Phe Thr Lys			
515	520	525	
ttt gct caa aca caa tct tta gcg acg aga agc tcg ggt ggt agt ggg			3308
Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser Gly			
530	535	540	545
ctt ggc ctc gcc atc tcc aag agg ttt gtg aat ctg atg gag ggt aac			3356
Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly Asn			
550	555	560	
att tgg att gag agc gat ggt ctt gga aaa gga tgc acg gct atc ttt			3404
Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile Phe			
565	570	575	
gat gtt aaa ctt ggg atc tca gaa cgt tca aac gaa tct aaa cag tcg			3452
Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln Ser			
580	585	590	
ggc ata ccg aaa gtt cca gcc att ccc cga cat tca aat ttc act gga			3500
Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr Gly			
595	600	605	
ctt aag gtt ctt gtc atg gat gag aac ggg gta agt aga atg gtg acg			3548
Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val Thr			
610	615	620	625
aag gga ctt ctt gta cac ctt ggg tgc gaa gtg acc acg gtg agt tca			3596
Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser Ser			
630	635	640	
aac gag gag tgt ctc cga gtt gtg tcc cat gag cac aaa gtg gtc ttc			3644
Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val Phe			
645	650	655	
atg gac gtg tgc atg ccc ggg gtc gaa aac tac caa atc gct ctc cgt			3692
Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu Arg			
660	665	670	
att cac gag aaa ttc aca aaa caa cgc cac caa cgg cca cta ctt gtg			3740
Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu Val			
675	680	685	
gca ctc agt ggt aac act gac aaa tcc aca aaa gag aaa tgc atg agc			3788
Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met Ser			
690	695	700	705

ttt ggt cta gac ggt gtg ttg ctc aaa ccc gta tca cta gac aac ata Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn Ile 710 . . . 715 . . . 720	3836
aga gat gtt ctg tct gat ctt ctc gag ccc cggtt tac gag ggc Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu Gly 725 . . . 730 . . . 735	3884
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aatgcatttcgac tttcatttcgac cacacaccag aatcctactg agttcgagta ttatggcatt ggggaaaactg tttttcttgtt accatttggtt gtgcttgtaa tttactgtgt tttttattcg gttttcgcta tcgaactgtg aaatggaaat ggatggagaa gagttaatga atgatatgg ccttttgcattt attctcaaatt taatattatt tggttttctt cttatttggtt gtgtgttggaa tttggaaatttta taagagatattt gcaaacattt tggtttgagt aaaaatgtgt caaatcgtgg cctctaatgatccgaaggtaa tatgaggagt aaaaacacttg tagttgtacc attatgctta ttcacttaggc aacaaatata ttttcagacc tagaaaaagct gcaaatgtta ctgaatacaa gtatgtcctc ttgtgttttta gacatttatg aactttcctt tatgttaattt tccagaatcc ttgtcagatt ctaatcatttgc ctttataattt atagttatac tcatggattt gtagttgagt atgaaaatatttttaatgc attttatgac ttgccaatttgc attgacaaca tgcataatc gacctgcaggc cactcgaagc ggccgcactt cgagtggaaat ctagctccc gatcctatct gtcaatttcat caaaaggaca gtagaaaaagg aaggtggcac tacaaatgcc atcattgcga taaaggaaag gctatcggtt aagatgcctc tgccgacagt ggtcccaaag atggaccccc acccacgagg agcatcggtt aaaaagaaga cgttccaaacc acgtcttcaa agcaagtgg ttgatgtgat acttccactg acgttaaggaa tgacgcacaa tcccactatc cttcgcaaga cccttcctct atataaggaa gttcatttca ttggagagg acacgctgaa atcaccagtc tctctctaca agatcggtt tctctagcta gacgatcggtt tcgcatttgcattt gaacaagatg gattgcacgc aggttctccg gccgcttggg tggagaggctt attcggttat gactggcac aacagacaat cggtcgctt gatgccgcgc tggtccggct gtcagcgcag gggcgcccg ttcttttgtt caagaccgac ctgtccgggtt ccctgaatga actgcaggac gaggcagcgc ggctatcggtt gctggccacg acgggcgttc ctgcgcagc tggctcgac gttgtcactg aagcggttggaaag ggactggctt gtttggcg aagtggccggg gcaggatctc ctgtcatctc 5140	5200

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